SEQUENCE LISTING

- (1) GENERAL INFORMATION
- (i) APPLICANT: Hillman, Jennifer L. Shah, Purvi
- (ii) TITLE OF THE INVENTION: NOVEL TUMOR SUPPRESSOR
- (iii) NUMBER OF SEQUENCES: 3
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Incyte Pharmaceuticals, Inc.
 - (B) STREET: 3174 Porter Drive
 - (C) CITY: Palo Alto
 - (D) STATE: CA
 - (E) COUNTRY: USA
 - (F) ZIP: 94304
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Diskette
 - (B) COMPUTER: IBM Compatible
 - (C) OPERATING SYSTEM: DOS
 - (D) SOFTWARE: FastSEQ for Windows Version 2.0
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: To Be Assigned
 - (B) FILING DATE: Filed Herewith
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Billings, Lucy J.
 - (B) REGISTRATION NUMBER: 36,749
 - (C) REFERENCE/DOCKET NUMBER: PF-0249 US
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 415-855-0555
 - (B) TELEFAX: 415-845-4166
 - (2) INFORMATION FOR SEQ ID NO:1:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 126 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: THPINOT03
 - (B) CLONE: 2446131

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- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
- Met Ser Tyr Lys Pro Ile Ala Pro Ala Pro Ser Xaa Thr Pro Gly Ser
- Ser Thr Pro Gly Pro Gly Thr Pro Val Pro Thr Gly Ser Val Pro Ser
- Pro Ser Gly Ser Val Pro Gly Ala Gly Ala Pro Phe Arg Pro Leu Phe 35 40 45
- Asn Asp Phe Gly Pro Pro Ser Met Gly Tyr Val Gln Ala Met Lys Pro

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Pro Gly Ala Gln Gly Ser Gln Ser Thr Tyr Thr Asp Leu Leu Ser Val

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Ile Glu Glu Met Gly Lys Glu Ile Arg Pro Thr Tyr Ala Gly Ser Lys
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Ser Ala Met Glu Arg Leu Lys Arg Gly Ile Ile Ile His Ala Arg Ala Leu
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(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 667 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: THPINOT03
- (B) CLONE: 2446131

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GGCTGAGCGG	CCCCGCAGCC	AACCCCCGAG	GAGCGGCCGG	CTGGCGTCCG	CCGCGCCCAG	60
GAGTTGGGGA	TGTCCTACAA	ACCCATCGCC	CCTGCTCCCA	GCAKCACCCC	TGGCTCCAGC	120
ACCCCTGGGC	CGGGCACCCC	GGTCCCTACA	GGAAGCGTCC	CGTCGCCGTC	GGGCTCAGTG	180
CCAGGAGCCG	GCGCTCCTTT	CAGACCGCTG	TTTAACGACT	TTGGACCGCC	TTCCATGGGC	240
TACGTGCAGG	CGATGAAGCC	ACCCGGCGCC	CAGGGCTCCC	AGAGCACCTA	CACGGACCTG	300
CTGTCAGTCA	TAGAGGAGAT	GGGCAAAGAG	ATCCGGCCTA	CCTATGCTGG	CAGCAAGAGC	360
GCCATGGAGC	GCCTGAAGAG	AGGTATCATC	CATGCCCGGG	CCCTAGTCAG	AGAGTGCCTG	420
GCAGAGACAG	AGCGGAACGC	CCGCACGTAA	CAGGAAGCGC	CTCGGCCTCA	GCGTCTGGAC	480
CTATCCGGCC	ACTGCAGAGC	ACCCGCTTCT	CCCTGGCCTT	CATCCCGAGT	TGCACTAACC	540
ATCCTGGGCT	TCCTGTCCTG	TGTCCCTTGG	TGGGTCCCCT	CCAGGAACCA	AGGAGTGGCC	600
CTCCAGGTGG	CAGCACTAAG	GACACCCCCC	CACAACAAGA	GTTAGCAGCG	AGGTCCCCAT	660
GAGTCCC						667

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 114 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GenBank
- (B) CLONE: 606837

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met 1	Ser	Tyr	Lys	Pro 5	Asn	Leu	Thr	Ala	His 10	Met	Pro	Ala	Ala	Ala 15	Leu
Asn	Ala	Gly	Ser 20	Val	His	Ser	Pro	Ser 25	Thr	Ser	Met	Ala	Thr 30	Ser	Ser
Gln	Tyr	Arg 35	Gln	Leu	Leu	Ser	Asp 40	Tyr	Gly	Pro	Pro	Ser 45	Leu	Gly	Tyr
Thr	Gln 50	Gly	Thr	Gly	Asn	Ser 55	Gln	Val	Pro	Gln	Ser 60	Lys	Tyr	Ala	Glu
Leu 65	Leu	Ala	Ile	Ile	Glu 70	Glu	Leu	Gly	Lys	Glu 75	Ile	Arg	Pro	Thr	Tyr 80
Ala	Gly	Ser	Lys	Ser 85	Ala	Met	Glu	Arg	Leu 90	Lys	Arg	Gly	Ile	Ile 95	His
Ala	Arg	Ser	Leu 100	Val	Arg	Glu	Cys	Leu 105	Ala	Glu	Thr	Glu	Arg 110	Asn	Ala
Arg	Ser														

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